AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently amended) A method for identifying a compound to treat a neuropsychiatric disorder, which method comprises:

(a) contacting a cell with a test compound;

(b) determining expression by the cell of one or more signature genes, wherein each said signature gene ~~comprising a nucleic acid that hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS:1-154 and the complements thereof~~ is differentially expressed in response to electroconvulsive seizure (ECS); and

(c) comparing the determined expression of the one or more signature genes to expression in a cell not contacted with the test compound,

wherein changes in expression of the one or more signature genes consistent with a therapeutic effect indicate that the test compound is useful for treating the neuropsychiatric disorder.

2. (Original) The method according to claim 1 in which the neuropsychiatric disorder is selected from the group consisting of, schizophrenia, autism, major depressive disorder (MDD), bipolar affective disorder (BAD), schizophrenia and psychotic depression.

3. (Original) The method according to claim 1 in which the cell is a neuronal cell.

4. (Original) The method according to claim 1, wherein changes in expression of signature genes which are similar to changes observed in ECS indicate that the test compound is useful for treating the disease or disorder.

5. (Original) The method according to claim 1, wherein changes in expression of signature genes which are similar to changes observed in ECT indicate that the test compound is useful for treating the disease or disorder.

6. (Original) The method according to claim 1, in which changes in the expression of signature genes are evaluated from a value (V) comprising the sum of each signature gene's change in expression.

7. (Original) The method according to claim 6, in which said value (V) is determined from the normalized change (E_i) in expression of each efficacy gene (i) weighted by the score value (ω_i) according to the relation: $V = \sum_i \omega_i E_i$.

8. (Original) A method for selecting one or more signature genes that are indicative of an effective therapy for treating a neuropsychiatric disorder, which method comprises identifying nucleic acids that are differentially expressed in an individual subjected to electroconvulsive seizure (ECS) compared to an individual not subjected to ECS.

9. (Original) The method according to claim 8 in which the neuropsychiatric disorder is selected from the group consisting of, schizophrenia, autism, major depressive disorder (MDD), bipolar affective disorder (BAD), schizophrenia and psychotic depression.

10. (Original) The method according to claim 8 wherein the individual is subjected to acute ECS.

11. (Original) The method according to claim 8 wherein the individual is subject to chronic ECS.

12. (Original) The method according to claim 8, wherein nucleic acids are identified that are differentially expressed in the hippocampus of an individual subjected to ECS compared to expression in the hippocampus of an individual not subjected to ECS.

13. (Original) The method according to claim 8, wherein nucleic acids are identified that are differentially expressed in the frontal cortex of an individual subjected to ECS compared to expression in the frontal cortex of an individual not subjected to ECS.

14. (Original) The method according to claim 8, wherein:

(a) a score value is obtained for each of the identified nucleic acids, the score value for each gene being a function of each gene's differential expression in individuals subjected to ECS, and

(b) signature genes are selected which have the highest score value.

15. (Original) The method according to claim 8, wherein nucleic acids that are differentially expressed comprise one or more nucleic acids that hybridize to a nucleic acid selected from the group consisting of SEQ ID NOS:1-154 or to a complement thereof.

16. (Original) A kit for detecting an ECS gene signature, wherein said kit comprises a plurality of oligonucleotides, each of which is capable of specifically hybridizing to a different ECS signature gene.

17. (Original) A kit according to claim 16, wherein each ECS signature gene is a nucleic acid having a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-152, a complement thereof or a homolog thereof.

18. (Original) A kit according to claim 17, wherein the ECS signature genes comprise at least one homolog of a sequence selected from the group consisting of SEQ ID NOS:1-152, or a complement thereof.

19. (Original) A kit according to claim 18, wherein said homolog specifically hybridizes from a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-152 and their complementary sequences.

20. (Original) A kit according to claim 18, wherein said homolog comprises a nucleotide sequence that is at least 80% identical to a nucleotide sequence selected from the group consisting of SEQ ID NOS:1-152 and their complementary sequences.

21. (Original) A kit according to claim 16, wherein each of the plurality of oligonucleotides is immobilized on a solid surface or support.

22. (Original) A kit according to claim 21, wherein each oligonucleotide is immobilized at a known position on the solid surface or support.

23. (Original) A kit according to claim 16, wherein at least some oligonucleotides in the plurality of oligonucleotides are capable of priming reverse transcription of an ECS signature gene.

24. (Original) A kit according to claim 23, further comprising a polymerase and nucleotide bases.

25. (Original) A kit according to claim 24 wherein the nucleotide bases are detectably labeled.

26. (Original) A kit according to claim 16 comprising oligonucleotides capable of specifically hybridizing to at least 10 different ECS signature genes.

27. (Original) A kit according to claim 16 comprising oligonucleotides capable of specifically hybridizing to at least 50 different ECS signature genes.

28. (Original) A kit according to claim 16 comprising oligonucleotides capable of specifically hybridizing to at least 100 different ECS signature genes.

29. (Original) A kit according to claim 16 comprising oligonucleotides capable of specifically hybridizing to at least 150 different ECS signature genes.

30. (New) The method according to claim 1, wherein each signature gene hybridizes to a nucleic acid having a sequence selected from the group consisting of SEQ ID NOS:1-154 and the complements thereof.

31. (New) The method according to claim 30, wherein each signature gene hybridizes to a nucleic acid having a sequence selected from the group consisting of SEQ ID NOS:1, 4, 15-17, 27, 43, 45, 53, 108, 145 and the complements thereof.

32. (New) The method according to claim 31, wherein said one or more signature genes include a signature gene that hybridizes to a nucleic acid having the sequence set forth in SEQ ID NO:145 or the complement thereof.

33. (New) The method according to claim 32, wherein said one or more signature genes also include signature genes that hybridize to

(i) nucleic acids having the sequences set forth in SEQ ID NOS:1, 4, 15-17, 27, 43, 45, 53, 108, and 145; or

(ii) the complements thereof.

34. (New) A method for identifying a compound to treat a neuropsychiatric disorder, which method comprises:

(a) contacting a cell with a test compound;

(b) determining expression by the cell of one or more signature genes, wherein each said signature gene comprising a nucleic acid that hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS:1, 4, 15-17, 27, 43, 45, 53, 108, 145 and the complements thereof; and

(c) comparing the determined expression of the one or more signature genes to expression in a cell not contacted with the test compound,

wherein changes in expression of the one or more signature genes consistent with a therapeutic effect indicate that the test compound is useful for treating the neuropsychiatric disorder.

35. (New) The method according to claim 34, wherein said one or more signature genes include a signature gene that hybridizes to a nucleic acid having the sequence set forth in SEQ ID NO:145 or the complement thereof.

36. (New) The method according to claim 35, wherein said one or more signature genes also include signature genes that hybridize to

(i) nucleic acids having the sequences set forth in SEQ ID NOS:1, 4, 15-17, 27, 43, 45, 53, 108, and 145; or

(ii) the complements thereof.

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